WHAT IS CLAIMED IS:

1. A method of genotyping, comprising the steps of:

(a) generating a first diversity panel from nucleic acid molecules of two or more organisms, wherein the first diversity panel comprises a reproducible pattern of nucleic acid molecules;

(b) separating the nucleic acid molecules of the first diversity panel on the basis of sequence or molecular weight;

(c) placing the separated nucleic acid molecules into an addressable array;

(d) generating a second diversity panel from nucleic acid molecules of an organism, wherein the second diversity panel comprises a reproducible pattern of nucleic acid molecules;

(e) hybridizing the second diversity panel to the addressable array; and

(f) detecting hybridization, therefrom determining a pattern of hybridization;

wherein the genotype of the second organism is determined from the hybridization pattern.

2. The method of claim 1, wherein the first diversity panel is generated by amplification.

3. The method of claim 1, wherein the second diversity panel is generated by amplification.

4. The method of claim 1, wherein the first diversity panel is cDNA.

5. The method of claim 1, wherein the second diversity panel further comprises a detectable molecule.

6. The method of claim 1, further comprising generating additional diversity panels, wherein each additional diversity panel is generated from nucleic acid molecules of an organism, wherein each diversity panel comprises a reproducible pattern of nucleic acid molecules.

7. The method of claim 6, wherein the second and additional diversity panels further comprise a detectable molecule, wherein the detectable molecule of each diversity panel can be distinguished from the detectable molecule of the other diversity panels.

8. The method of either one of claims 4 or 6, wherein the detectable molecule is selected from the group consisting of a fluorochrome, a mass spectrometry tag, a chemiluminescent molecule and a radioactive molecule.

9. The method of either one of claims 2 or 3, wherein the amplification is performed using a single primer.

10. The method of either one of claims 2 or 3, wherein the amplification is performed using a primer pair, wherein one of the primers anneals to a sequence that is conserved among a family of insertion elements.

11. The method of claim 1, wherein the first or second or both diversity panels are generated by the steps comprising: digesting the nucleic acids of the organisms with one or more restriction enzymes to generate fragments, ligating adapter sequences to the fragments, and amplifying the ligated fragments using a primer that anneals to the adapter sequence.

12. The method of claim 11, wherein the restriction enzyme is methylation sensitive.

13. The method of claim 1, wherein the first or second or both diversity panels are generated by the steps comprising: digesting the nucleic acids of the organisms with a restriction enzyme to generate fragments, ligating an adapter sequence to the fragments, and amplifying the ligated fragments using a primer pair, wherein one primer anneals to at least part of the adapter sequence and the other primer anneals to a sequence that is conserved among a family of insertion elements.

14. The method of claim 1, wherein the first or second or both diversity panels are generated by digestion of the nucleic acid molecules with one or more restriction enzymes and size selection of the digested nucleic acids.

15. The method of either of claims 2 or 3, wherein the amplification method is amplified fragment-length polymorphism (AFLP) or random-amplified polymorphic DNA (RAPD).

16. The method of claim 1, wherein the nucleic acid of the organisms is genomic DNA, mitochondrial DNA, chloroplast DNA or mRNA.

17. The method of claim 1, wherein the organism of step (d) is the same as one of the organisms of step (a).

18. The method of claim 1, wherein the organisms of step (a) are from the same species.

19. The method of claim 1, wherein the organisms of step (a) are selected from the group consisting of plants, bacteria, viruses, fungi, animals and humans.

20. The method of claim 1, wherein the organisms of step (a) are plants selected from the group consisting of wheat, rice, corn, barley,

Arabidopsis, potato, cassava, banana, yam, cowpea, apple, pear, orange, walnut, brazil nut, pecan, lentil, pea and rye.

21. The method of claim 1, wherein the addressable array is on a silicon chip or a glass slide.

22. The method of claim 1, wherein the detecting step detects the presence or absence of hybridization.

23. A method of genotyping, comprising the steps of:

(a) amplifying regions of nucleic acid molecules isolated from two or more organisms to generate a first set of amplified regions, such that reproducible patterns are produced, wherein the amplification is performed on a mixture of the nucleic acids;

(b) cloning the first set of amplified regions to generate clones;

(c) placing individual clones into an addressable array;

(d) amplifying regions of nucleic acid isolated from one selected organism of step (a) to generate a second set of amplified regions, wherein the second set of amplified regions include a detectable marker;

(e) hybridizing the second set of amplified regions to the addressable array;

(f) detecting hybridization, therefrom determining a pattern of hybridization;

wherein the genotype of the selected organism of step (d) is determined from the hybridization pattern.

24. A method of genotyping, comprising the steps of:

(a) amplifying regions of nucleic acid molecules isolated from two or more organisms to generate a first set of amplified regions,

such that reproducible patterns are produced, wherein the amplification is performed on a mixture of the nucleic acids;

(b) cloning the first set of amplified regions to generate clones;

(c) placing individual clones into an addressable array;

(d) amplifying regions of nucleic acid isolated from nucleic acid molecules of an organism to generate a second set of amplified regions, wherein the amplification is performed using a primer pair in which one of the primers anneals to a sequence that is conserved among a family of insertion elements; and wherein the second set of amplified regions include a detectable marker;

(e) hybridizing the second set of amplified regions to the addressable array;

(f) detecting hybridization, therefrom determining a pattern of hybridization;

wherein the genotype of the organism of step (d) is determined from the hybridization pattern.

25. A method of genotyping, comprising the steps of:

(a) generating a first diversity panel from nucleic acid molecules isolated from two or more organisms by digesting the nucleic acids with one or more methylation sensitive restriction enzymes to generate fragments, ligating adapter sequences to the fragments, and amplifying the ligated fragments using a primer that anneals to the adapter sequence;

(b) cloning the first diversity panel to generate clones;

(c) placing individual clones into an addressable array;

(d) generating a second diversity panel from nucleic acid molecules isolated from an organism by digesting the nucleic acids with one or more methylation sensitive restriction enzymes to generate

fragments, ligating adapter sequences to the fragments, and amplifying the ligated fragments using a primer that anneals to the adapter sequence, wherein the second set of amplified regions include a detectable marker;

(e) hybridizing the second diversity panel to the addressable array;

(f) detecting hybridization, therefrom determining a pattern of hybridization;

wherein the genotype of the selected organism of step (d) is determined from the hybridization pattern.

26. A method of identifying a nucleic acid molecule containing a polymorphism, comprising the steps of:

(a) separately amplifying regions of nucleic acid isolated from a first organism and a second organism to generate a first set and a second set of amplified regions, wherein the second set of amplified regions include a detectable marker;

(b) cloning the first set of amplified regions ;

(c) placing individual clones into an addressable array;

(d) hybridizing the second set of amplified regions to the array of step (c);

(e) identifying a clone that does not detectably hybridize with the second set of amplified regions;

thereby identifying a clone that contains a polymorphism.

27. The method of claim 26, further comprising isolating clones that contain a polymorphism.

28. The method of claim 27, further comprising placing the isolated clones into an addressable array.

29. The method of claim 28, further comprising generating a diversity panel from nucleic acid molecules of two or more organisms, wherein the diversity panel comprises a reproducible pattern of nucleic acid molecules, and hybridizing the diversity panel to the addressable array of claim 28.

30. The method of claim 27, further comprising mapping the clone to a genomic region.

31. A method of identifying a nucleic acid molecule containing a polymorphism, comprising the steps of:

(a) amplifying regions of nucleic acid isolated from a first organism to generate a first set of amplified regions;

(b) cloning the amplified regions from the first set of amplified regions to generate clones;

(c) placing individual clones into an addressable array;

(d) amplifying regions of a mixture of nucleic acids isolated from two or more organisms to generate a second set of amplified regions;

(e) hybridizing the second set of amplified regions to the array of step (c);

(f) identifying a clone that does not detectably hybridize with the amplified regions from the second organism;

thereby identifying a nucleic acid molecule that contains a polymorphism.

32. The method of claim 31, further comprising isolating the clone identified in step (f).

33. The method of claim 32, further comprising placing the isolated clones into an addressable array.

34. The method of claim 33, further comprising generating a diversity panel from nucleic acid molecules of two or more organisms, wherein the diversity panel comprises a reproducible pattern of nucleic acid molecules, and hybridizing the diversity panel to the addressable array of claim 30.

35. The method of claim 32, further comprising mapping the clone to a genomic region.

36. A kit for genotyping, comprising an addressable array of DNA molecules that comprises a diversity panel generated from nucleic acid molecules of two or more organisms, wherein the diversity panel comprises a reproducible pattern of nucleic acid molecules.

37. The kit of claim 36, further comprising a pair of amplification primers.

38. An ordered array of DNA molecules, wherein the DNA molecules are generated by a method comprising amplification of a mixture of nucleic acids isolated from two or more organisms.

39. An ordered array of DNA molecules, wherein the DNA molecules are generated by a method comprising restriction enzyme digestion with a methylation sensitive enzyme of a mixture of nucleic acids isolated from two or more organisms.

40. An ordered array of DNA molecules, wherein the DNA molecules are generated by a method comprising amplification of a mixture of nucleic acids isolated from two or more organisms, wherein the amplification uses a primer pair in which one primer anneals to a sequence that is conserved among a family of insertion elements.